

## Murphy, Joseph

---

**Fr m:** Murphy, Joseph  
**Sent:** Wednesday, June 05, 2002 10:57 AM  
**T :** STIC-Biotech/ChemLib  
**Subject:** 09710419

STIC/Biotech:

Please search SEQ ID NO: 13 against protein databases.

Please include and interference search of SEQ ID NO: 13.

Please send the results on DISK.

Thanks a lot...

Joseph F. Murphy, Ph.D.  
Patent Examiner, Art Unit 1646  
joseph.murphy@uspto.gov  
CM1 9A01  
Mailbox: 10C01  
(703) 305-7245

## 09710419 Results

SEQ ID NO: 13

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	103	96.3	27	18	AAW22819	M2GlyR based chann
2	103	96.3	28	18	AAW22820	M2GlyR based chann
3	103	96.3	29	18	AAW22821	M2GlyR based chann
4	98	91.6	26	18	AAW22818	M2GlyR based chann
5	93	86.9	25	18	AAW22817	M2GlyR based chann
6	88	82.2	24	18	AAW22816	M2GlyR based chann
7	87	81.3	25	18	AAW22815	M2GlyR based chann
8	83	77.6	23	18	AAW22803	Channel-forming M2
9	83	77.6	23	18	AAW22812	M2GlyR based chann
10	83	77.6	24	18	AAW22813	M2GlyR based chann
11	83	77.6	24	18	AAW22814	M2GlyR based chann
12	83	77.6	26	18	AAW22822	M2GlyR based chann
13	83	77.6	27	18	AAW22823	M2GlyR based chann
14	83	77.6	27	18	AAW22809	Channel-forming pe
15	83	77.6	417	21	AAB19336	Amino acid sequenc
16	77	72.0	23	18	AAW22810	M2GlyR based chann
17	77	72.0	61	22	AAM33425	Peptide #7462 enco
18	77	72.0	637	21	AAY51077	D. simulans GABA r
19	76	71.0	23	18	AAW22811	M2GlyR based chann
20	72	67.3	452	17	AAR97299	Human GABA-A recep
21	72	67.3	467	16	AAR83968	GABA-A receptor ga
22	71	66.4	453	14	AAR31187	GABA-A receptor al
23	71	66.4	453	15	AAR59865	Human GABA recepto
24	71	66.4	459	20	AAW81636	GABA-gated chlorid
25	71	66.4	467	20	AAW81634	GABA-gated chlorid
26	71	66.4	467	22	AAM39221	Human polypeptide
27	71	66.4	481	20	AAW81635	GABA-gated chlorid
28	71	66.4	488	19	AAW69285	GABA gated chlorid
29	71	66.4	488	19	AAW69286	GABA gated chlorid
30	71	66.4	489	22	AAM41007	Human polypeptide
31	71	66.4	496	20	AAW81633	GABA-gated chlorid
32	71	66.4	561	19	AAW97413	Lucilia cuprina GA
33	71	66.4	637	14	AAR34035	Sequence of a GABA
34	71	66.4	637	21	AAY51074	D. melanogaster po
35	71	66.4	637	21	AAY51075	D. melanogaster GA
36	71	66.4	637	21	AAY51076	D. melanogaster GA
37	69	64.5	222	20	AAW81637	GABA-gated chlorid
38	69	64.5	345	22	AAU04471	Human gamma-amino
39	69	64.5	392	22	AAU04468	Human gamma-amino
40	69	64.5	420	22	AAU04470	Human gamma-amino
41	69	64.5	467	22	AAU04467	Human gamma-amino
42	67	62.6	554	17	AAR97298	Human GABA-A recep
43	66	61.7	474	22	AAM39098	Human polypeptide
44	66	61.7	478	22	AAM40884	Human polypeptide
45	66	61.7	496	17	AAR89336	GABA receptor subu

Issued:

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	103	96.3	27	3	US-09-093-227-17	Sequence 17, Appl
2	103	96.3	28	3	US-09-093-227-18	Sequence 18, Appl

3	103	96.3	29	3	US-09-093-227-19	Sequence 19, Appl
4	98	91.6	26	3	US-09-093-227-16	Sequence 16, Appl
5	93	86.9	25	3	US-09-093-227-15	Sequence 15, Appl
6	88	82.2	24	3	US-09-093-227-14	Sequence 14, Appl
7	87	81.3	25	3	US-09-093-227-13	Sequence 13, Appl
8	83	77.6	23	3	US-09-093-227-1	Sequence 1, Appli
9	83	77.6	23	3	US-09-093-227-10	Sequence 10, Appl
10	83	77.6	24	3	US-09-093-227-11	Sequence 11, Appl
11	83	77.6	24	3	US-09-093-227-12	Sequence 12, Appl
12	83	77.6	26	3	US-09-093-227-20	Sequence 20, Appl
13	83	77.6	27	3	US-09-093-227-7	Sequence 7, Appli
14	83	77.6	27	3	US-09-093-227-21	Sequence 21, Appl
15	83	77.6	57	1	US-08-137-614A-23	Sequence 23, Appl
16	77	72.0	23	3	US-09-093-227-8	Sequence 8, Appli
17	77	72.0	637	3	US-08-072-064-8	Sequence 8, Appli
18	76	71.0	23	3	US-09-093-227-9	Sequence 9, Appli
19	72	67.3	57	1	US-08-137-614A-22	Sequence 22, Appl
20	71	66.4	52	1	US-08-137-614A-15	Sequence 15, Appl
21	71	66.4	453	1	US-08-417-330A-18	Sequence 18, Appl
22	71	66.4	467	1	US-08-459-100A-3	Sequence 3, Appli
23	71	66.4	488	1	US-08-554-659-2	Sequence 2, Appli
24	71	66.4	488	1	US-08-554-659-4	Sequence 4, Appli
25	71	66.4	617	1	US-08-137-614A-26	Sequence 26, Appl
26	71	66.4	637	3	US-08-072-064-1	Sequence 1, Appli
27	71	66.4	637	3	US-08-072-064-4	Sequence 4, Appli
28	71	66.4	637	3	US-08-072-064-6	Sequence 6, Appli
29	71	66.4	637	5	PCT-US92-08558-1	Sequence 1, Appli
30	70	65.4	57	1	US-08-137-614A-21	Sequence 21, Appl
31	66	61.7	57	1	US-08-137-614A-17	Sequence 17, Appl
32	66	61.7	57	1	US-08-137-614A-18	Sequence 18, Appl
33	66	61.7	57	1	US-08-137-614A-20	Sequence 20, Appl
34	66	61.7	474	1	US-08-459-100A-4	Sequence 4, Appli
35	66	61.7	496	1	US-08-137-614A-2	Sequence 2, Appli
36	66	61.7	496	2	US-08-768-301-2	Sequence 2, Appli
37	66	61.7	510	1	US-08-249-112-3	Sequence 3, Appli
38	66	61.7	510	5	PCT-US95-06556-3	Sequence 3, Appli
39	66	61.7	617	1	US-08-137-614A-24	Sequence 24, Appl
40	66	61.7	617	1	US-08-137-614A-25	Sequence 25, Appl
41	65	60.7	50	1	US-08-435-933-3	Sequence 3, Appli
42	65	60.7	50	5	PCT-US96-06035-3	Sequence 3, Appli
43	65	60.7	456	1	US-08-435-933-6	Sequence 6, Appli
44	65	60.7	456	5	PCT-US96-06035-6	Sequence 6, Appli
45	65	60.7	474	1	US-08-417-330A-20	Sequence 20, Appl

#### SUMMARIES

SUMMARIES						
Result	Query			DB	ID	Description
	No.	Score	Match Length			
1	83	77.6	337	2	A49970	glycine receptor a
2	83	77.6	449	2	S12382	glycine receptor a
3	83	77.6	451	2	C49970	glycine receptor a
4	83	77.6	457	2	S20662	glycine receptor a
5	79	73.8	1106	2	T25065	hypothetical prote
6	77	72.0	451	2	B49970	glycine receptor a
7	77	72.0	452	2	S14816	glycine receptor a
8	77	72.0	452	2	S12381	glycine receptor a
9	77	72.0	452	2	S18836	glycine receptor a
10	77	72.0	464	2	A23682	glycine receptor a
11	73	68.2	465	2	A38079	gamma-aminobutyric
12	72	67.3	449	2	A36303	gamma-aminobutyric
13	72	67.3	449	2	I52630	GABAA receptor del
14	72	67.3	449	2	A34625	gamma-aminobutyric
15	71	66.4	210	2	JH0794	gamma-aminobutyric
16	71	66.4	464	2	JH0824	gamma-aminobutyric
17	71	66.4	465	2	S12056	gamma-aminobutyric
18	71	66.4	466	2	JQ0077	gamma-aminobutyric

19	71	66.4	466	2	JH0316	gamma-aminobutyric
20	71	66.4	467	2	S03905	gamma-aminobutyric
21	71	66.4	474	2	JH0317	gamma-aminobutyric
22	71	66.4	474	2	S13086	gamma-aminobutyric
23	71	66.4	475	2	B39272	gamma-aminobutyric
24	71	66.4	478	2	T24805	hypothetical prote
25	71	66.4	533	2	S33744	cyclodiene insecti
26	70	65.4	457	2	S38296	gamma-aminobutyric
27	70	65.4	467	2	S16915	gamma-aminobutyric
28	70	65.4	467	2	S19317	gamma-aminobutyric
29	69	64.5	464	2	S65756	gamma-aminobutyric
30	67	62.6	443	2	S11396	gamma-aminobutyric
31	67	62.6	453	2	S11087	gamma-aminobutyric
32	67	62.6	473	2	A38627	gamma-aminobutyric
33	67	62.6	552	2	S17551	gamma-aminobutyric
34	67	62.6	554	2	G01928	gamma-aminobutyric
35	67	62.6	556	2	S06838	gamma-aminobutyric
36	66	61.7	461	2	S50864	avermectin-sensiti
37	66	61.7	474	2	B60039	gamma-aminobutyric
38	66	61.7	474	2	A40336	gamma-aminobutyric
39	66	61.7	474	2	S53530	gamma-aminobutyric
40	66	61.7	474	2	B27142	gamma-aminobutyric
41	66	61.7	495	2	T20754	hypothetical prote
42	66	61.7	496	2	JN0603	gamma-aminobutyric
43	66	61.7	499	2	S17785	gamma-aminobutyric
44	66	61.7	545	2	T27614	hypothetical prote
45	65	60.7	437	2	S34469	gamma-aminobutyric

#### SUMMARIES

SEQUENCES							
Result	% Query		Length	DB	ID	Description	
No.	Score	Match					
1	83	77.6	337	1	GRA4_MOUSE	Q61603 mus musculu	
2	83	77.6	444	1	GRA1_BRARE	O93430 brachydanio	
3	83	77.6	449	1	GRA1_HUMAN	P23415 homo sapien	
4	83	77.6	457	1	GRA1_BOVIN	P57695 bos taurus	
5	83	77.6	457	1	GRA1_MOUSE	Q64018 mus musculu	
6	83	77.6	457	1	GRA1_RAT	P07727 rattus norv	
7	77	72.0	452	1	GRA2_HUMAN	P23416 homo sapien	
8	77	72.0	452	1	GRA2_RAT	P22771 rattus norv	
9	77	72.0	464	1	GRA3_RAT	P24524 rattus norv	
10	77	72.0	465	1	GRA3_HUMAN	O75311 homo sapien	
11	73	68.2	465	1	GAR2_HUMAN	P28476 homo sapien	
12	72	67.3	449	1	GAD_MOUSE	P22933 mus musculu	
13	72	67.3	449	1	GAD_RAT	P18506 rattus norv	
14	72	67.3	452	1	GAD_HUMAN	O14764 homo sapien	
15	72	67.3	467	1	GAC3_HUMAN	Q99928 homo sapien	
16	71	66.4	465	1	GAC1_MOUSE	Q9r0y8 mus musculu	
17	71	66.4	465	1	GAC1_RAT	P23574 rattus norv	
18	71	66.4	466	1	GAC2_RAT	P18508 rattus norv	
19	71	66.4	467	1	GAC2_HUMAN	P18507 homo sapien	
20	71	66.4	474	1	GAC2_CHICK	P21548 gallus gall	
21	71	66.4	474	1	GAC2_MOUSE	P22723 mus musculu	
22	71	66.4	475	1	GAC2_BOVIN	P22300 bos taurus	
23	71	66.4	606	1	GAB_DROME	P25123 drosophila	
24	70	65.4	457	1	GAC4_CHICK	P34904 gallus gall	
25	70	65.4	467	1	GAC3_MOUSE	P27681 mus musculu	
26	70	65.4	467	1	GAC3_RAT	P28473 rattus norv	
27	69	64.5	464	1	GAR3_RAT	P50573 rattus norv	
28	67	62.6	453	1	GAA6_HUMAN	Q16445 homo sapien	
29	67	62.6	453	1	GAA6_MOUSE	P16305 mus musculu	
30	67	62.6	453	1	GAA6_RAT	P30191 rattus norv	
31	67	62.6	465	1	GAA6_CHICK	Q90845 gallus gall	
32	67	62.6	473	1	GAR1_HUMAN	P24046 homo sapien	
33	67	62.6	474	1	GAR1_MOUSE	P56475 mus musculu	
34	67	62.6	474	1	GAR1_RAT	P50572 rattus norv	

35	67	62.6	552	1	GAA4_MOUSE	Q9d6f4 mus musculu
36	67	62.6	552	1	GAA4_RAT	P28471 rattus norv
37	67	62.6	554	1	GAA4_HUMAN	P48169 homo sapien
38	67	62.6	556	1	GAA4_BOVIN	P20237 bos taurus
39	66	61.7	474	1	GAB1_BOVIN	P08220 bos taurus
40	66	61.7	474	1	GAB1_HUMAN	P18505 homo sapien
41	66	61.7	474	1	GAB1_MOUSE	P50571 mus musculu
42	66	61.7	474	1	GAB1_RAT	P15431 rattus norv
43	66	61.7	496	1	GAB3_DROME	Q08832 drosophila
44	66	61.7	499	1	GAB_LYMST	P26714 lymnaea sta
45	65	60.7	473	1	GAB3_HUMAN	P28472 homo sapien

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	83	77.6	449	6	Q9GKF0	Q9gkf0 bos taurus
2	83	77.6	456	13	Q9DES9	Q9des9 brachydanio
3	83	77.6	457	6	Q9GKE9	Q9gke9 bos taurus
4	79	73.8	475	5	Q9Y0I4	Q9y0i4 caenorhabdi
5	79	73.8	487	5	Q9Y0I5	Q9y0i5 caenorhabdi
6	79	73.8	506	5	Q9Y0I3	Q9y0i3 caenorhabdi
7	79	73.8	1106	5	Q22637	Q22637 caenorhabdi
8	77	72.0	147	11	Q9JL29	Q9j129 mus musculu
9	77	72.0	219	4	Q9UPF3	Q9upf3 homo sapien
10	77	72.0	480	11	Q99JC9	Q99jc9 rattus norv
11	73	68.2	416	5	Q17367	Q17367 caenorhabdi
12	73	68.2	421	5	O46123	O46123 haemonchus
13	73	68.2	654	5	O01436	O01436 caenorhabdi
14	71	66.4	141	5	Q26435	Q26435 tribolium c
15	71	66.4	254	5	Q26410	Q26410 blattella g
16	71	66.4	256	5	Q26409	Q26409 blattella g
17	71	66.4	274	5	Q26411	Q26411 blattella g
18	71	66.4	276	5	Q26412	Q26412 blattella g
19	71	66.4	351	5	Q25634	Q25634 onchocerca
20	71	66.4	365	5	O77249	O77249 apis mellif
21	71	66.4	379	5	O96964	O96964 ascaris suu
22	71	66.4	430	5	Q17369	Q17369 caenorhabdi
23	71	66.4	438	5	O46124	O46124 haemonchus
24	71	66.4	444	5	O76472	O76472 musca domes
25	71	66.4	478	5	O17548	O17548 caenorhabdi
26	71	66.4	481	5	O18471	O18471 heliothis v
27	71	66.4	487	5	Q9Y0I6	Q9y0i6 caenorhabdi
28	71	66.4	494	5	Q9XZW0	Q9xzw0 heliothis v
29	71	66.4	496	5	O18468	O18468 heliothis v
30	71	66.4	533	5	Q16896	Q16896 aedes aegyp
31	71	66.4	541	5	Q9U9B8	Q9u9b8 ceratitidis c
32	71	66.4	550	5	O17145	O17145 lucilia cup
33	71	66.4	601	5	P92138	P92138 drosophila
34	71	66.4	606	5	Q9VSV0	Q9vsv0 drosophila
35	71	66.4	606	5	Q9BLY8	Q9bly8 drosophila
36	71	66.4	657	5	O17547	O17547 caenorhabdi
37	71	66.4	657	5	Q9TW41	Q9tw41 caenorhabdi
38	70	65.4	435	5	Q9TZR3	Q9tzt3 haemonchus
39	70	65.4	435	5	Q9TYG6	Q9tyg6 haemonchus
40	70	65.4	435	5	Q9GQW8	Q9gqw8 haemonchus
41	69	64.5	223	5	O18469	O18469 heliothis v
42	69	64.5	470	13	Q9YGQ2	Q9ygg2 morone amer
43	69	64.5	473	13	O42157	O42157 morone amer
44	69	64.5	479	13	Q9YGQ5	Q9ygg5 morone amer
45	68	63.6	484	5	Q9U990	Q9u990 caenorhabdi

SEQ ID NO: 1

# SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	110	100.0	23	18	AAW22803	Channel-forming M2
	2	110	100.0	23	18	AAW22812	M2GlyR based chann
	3	110	100.0	24	18	AAW22813	M2GlyR based chann
	4	110	100.0	24	18	AAW22814	M2GlyR based chann
	5	110	100.0	24	18	AAW22816	M2GlyR based chann
	6	110	100.0	25	18	AAW22815	M2GlyR based chann
	7	110	100.0	25	18	AAW22817	M2GlyR based chann
	8	110	100.0	26	18	AAW22818	M2GlyR based chann
	9	110	100.0	26	18	AAW22822	M2GlyR based chann
	10	110	100.0	27	18	AAW22819	M2GlyR based chann
	11	110	100.0	27	18	AAW22823	M2GlyR based chann
	12	110	100.0	27	18	AAW22809	Channel-forming pe
	13	110	100.0	28	18	AAW22820	M2GlyR based chann
	14	110	100.0	29	18	AAW22821	M2GlyR based chann
	15	110	100.0	417	21	AAB19336	Amino acid sequenc
	16	104	94.5	23	18	AAW22810	M2GlyR based chann
	17	104	94.5	61	22	AAM33425	Peptide #7462 enco
	18	103	93.6	23	18	AAW22811	M2GlyR based chann
	19	83	75.5	637	21	AAV51077	D. simulans GABA r
	20	81	73.6	50	17	AAW05247	Glutamate-gated ch
	21	81	73.6	455	20	AAW97860	Cat flea glutamate
	22	81	73.6	456	17	AAW05246	Drosophila glutama
	23	81	73.6	462	22	AAE00863	Short form of S. a
	24	81	73.6	462	22	AAE00864	Short form of S. a
	25	81	73.6	513	22	AAE00861	Long form of S. am
	26	81	73.6	513	22	AAE00862	Long form of S. am
	27	77	70.0	459	20	AAW81636	GABA-gated chlorid
	28	77	70.0	467	20	AAW81634	GABA-gated chlorid
	29	77	70.0	481	20	AAW81635	GABA-gated chlorid
	30	77	70.0	488	19	AAW69285	GABA gated chlorid
	31	77	70.0	488	19	AAW69286	GABA gated chlorid
	32	77	70.0	496	17	AAR89336	GABA receptor subu
	33	77	70.0	496	20	AAW86161	Insect GABA recept
	34	77	70.0	496	20	AAW81633	GABA-gated chlorid
	35	77	70.0	510	17	AAR88360	Caenorhabditis ele
	36	77	70.0	561	19	AAW97413	Lucilia cuprina GA
	37	77	70.0	637	14	AAR34035	Sequence of a GABA
	38	77	70.0	637	21	AAV51074	D. melanogaster po
	39	77	70.0	637	21	AAV51075	D. melanogaster GA
	40	77	70.0	637	21	AAV51076	D. melanogaster GA
	41	75	68.2	222	20	AAW81637	GABA-gated chlorid
	42	74	67.3	452	17	AAR97299	Human GABA-A recep
	43	73	66.4	467	16	AAR83968	GABA-A receptor ga
	44	73	66.4	467	22	AAM39221	Human polypeptide
	45	73	66.4	489	22	AAM41007	Human polypeptide

RESULT 1

AAW22803

ID AAW22803 standard; peptide; 23 AA.

XX

AC AAW22803;

XX

DT 13-MAR-1998 (first entry)

XX

DE Channel-forming M2GlyR peptide 1.

XX

KW Channel-forming peptide; channel assembly; epithelial cell; treatment;

KW cystic fibrosis; polycystic kidney disease; anion transportation; M2GlyR.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9726905-A1.  
 XX  
 PD 31-JUL-1997.  
 XX  
 PF 27-JAN-1997; 97WO-US01103.  
 XX  
 PR 24-JAN-1997; 97US-0789155.  
 PR 25-JAN-1996; 96US-0591381.  
 PR 23-JAN-1997; 97US-0591381.  
 XX  
 PA (UNIV ) UNIV KANSAS MEDICAL CENT.  
 PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
 XX  
 PI Iwamoto T, Sullivan LP, Tomich JM;  
 XX  
 DR WPI; 1997-393366/36.  
 XX  
 PT Channel assembly for transporting ions across epithelial cell  
 PT membranes - comprises new water soluble peptide(s), for treating  
 PT cystic fibrosis and polycystic kidney disease by altering water flux  
 PT across cells  
 XX  
 PS Claim 31; Page 50; 93pp; English.  
 XX  
 CC This M2GlyR peptide is a channel-forming amphipathic helical segment. It  
 CC has the amino acid sequence of the putative transmembrane segment M2 of  
 CC the strychnine-binding alpha subunit of the inhibitory glycine receptor.  
 CC This is used to construct a novel channel assembly, comprising 3-6 novel  
 CC peptides, of 18-30 amino acids. The peptides are synthesized by standard  
 CC solid phase peptide synthesis. The peptides are water soluble to at  
 CC least 10 mM and enables anions to be transported through a membrane of  
 CC an epithelial cell when they are embedded in the membrane. The channel  
 CC assembly can be used to alter the flux of water across an epithelial  
 CC cell, particularly for treatment of cystic fibrosis (where affected cells  
 CC are in the airway, pancreatic duct or epididymis). The channel assembly  
 CC can also be used in the treatment of autosomal dominant polycystic kidney  
 CC disease (where the affected cells are in the cystic epithelium). The  
 CC channel assembly spontaneously inserts into the basolateral membrane to  
 CC prevent water flow to adjacent cysts.  
 XX  
 SQ Sequence 23 AA;

Query Match 100.0%; Score 110; DB 18; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PARVGLGITTTLMTTQSSGSRA 23  
 |||||  
 Db 1 parvglgitttlmttgssgsra 23

Issued:

#### SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	110	100.0	23	3	US-09-093-227-1
2	110	100.0	23	3	US-09-093-227-10
3	110	100.0	24	3	US-09-093-227-11
4	110	100.0	24	3	US-09-093-227-12
5	110	100.0	24	3	US-09-093-227-14
6	110	100.0	25	3	US-09-093-227-13
7	110	100.0	25	3	US-09-093-227-15
8	110	100.0	26	3	US-09-093-227-16
9	110	100.0	26	3	US-09-093-227-20
10	110	100.0	27	3	US-09-093-227-7

11	110	100.0	27	3	US-09-093-227-17	Sequence 17, Appl
12	110	100.0	27	3	US-09-093-227-21	Sequence 21, Appl
13	110	100.0	28	3	US-09-093-227-18	Sequence 18, Appl
14	110	100.0	29	3	US-09-093-227-19	Sequence 19, Appl
15	110	100.0	57	1	US-08-137-614A-23	Sequence 23, Appl
16	104	94.5	23	3	US-09-093-227-8	Sequence 8, Appli
17	103	93.6	23	3	US-09-093-227-9	Sequence 9, Appli
18	83	75.5	637	3	US-08-072-064-8	Sequence 8, Appli
19	81	73.6	50	1	US-08-435-933-3	Sequence 3, Appli
20	81	73.6	50	5	PCT-US96-06035-3	Sequence 3, Appli
21	81	73.6	456	1	US-08-435-933-6	Sequence 6, Appli
22	81	73.6	456	5	PCT-US96-06035-6	Sequence 6, Appli
23	77	70.0	52	1	US-08-137-614A-15	Sequence 15, Appl
24	77	70.0	57	1	US-08-137-614A-17	Sequence 17, Appl
25	77	70.0	57	1	US-08-137-614A-18	Sequence 18, Appl
26	77	70.0	488	1	US-08-554-659-2	Sequence 2, Appli
27	77	70.0	488	1	US-08-554-659-4	Sequence 4, Appli
28	77	70.0	496	1	US-08-137-614A-2	Sequence 2, Appli
29	77	70.0	496	2	US-08-768-301-2	Sequence 2, Appli
30	77	70.0	510	1	US-08-249-112-3	Sequence 3, Appli
31	77	70.0	510	5	PCT-US95-06556-3	Sequence 3, Appli
32	77	70.0	617	1	US-08-137-614A-24	Sequence 24, Appl
33	77	70.0	617	1	US-08-137-614A-26	Sequence 26, Appl
34	77	70.0	637	3	US-08-072-064-1	Sequence 1, Appli
35	77	70.0	637	3	US-08-072-064-4	Sequence 4, Appli
36	77	70.0	637	3	US-08-072-064-6	Sequence 6, Appli
37	77	70.0	637	5	PCT-US92-08558-1	Sequence 1, Appli
38	74	67.3	57	1	US-08-137-614A-22	Sequence 22, Appl
39	73	66.4	57	1	US-08-137-614A-21	Sequence 21, Appl
40	73	66.4	467	1	US-08-459-100A-3	Sequence 3, Appli
41	71	64.5	453	1	US-08-417-330A-18	Sequence 18, Appl
42	68	61.8	57	1	US-08-137-614A-20	Sequence 20, Appl
43	68	61.8	440	1	US-08-459-100A-2	Sequence 2, Appli
44	68	61.8	440	5	PCT-US94-09589-2	Sequence 2, Appli
45	68	61.8	474	1	US-08-459-100A-4	Sequence 4, Appli

RESULT 3

US-09-093-227-11

; Sequence 11, Application US/09093227

; Patent No. 6077826

; GENERAL INFORMATION:

; APPLICANT: Tomich, John M.

; APPLICANT: Iwamoto, Takeo

; APPLICANT: Sullivan, Lawrence P.

; TITLE OF INVENTION: A Synthetic Macromolecular Channel

; TITLE OF INVENTION: Assembly for Transport of Chloride Ions through Epithelium

; TITLE OF INVENTION: Useful in Treating Cystic Fibrosis

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hovey, Williams, Timmons & Collins

; STREET: 2405 Grand Blvd., Ste. 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: USA

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/093,227

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/789,155

; FILING DATE: January 24, 1997

; CLASSIFICATION:



```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Collins, John M.
;   REGISTRATION NUMBER: 26,262
;   REFERENCE/DOCKET NUMBER: 23867B
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (816) 474-9050
;   TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 24 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   FRAGMENT TYPE: internal
;   ORIGINAL SOURCE:
;     TISSUE TYPE: Brain
;   FEATURE:
;     NAME/KEY: Modified-site
;     LOCATION: 1
;     OTHER INFORMATION: /note= "N-terminus is capped with
;     OTHER INFORMATION: Acetyl group. Xaa at position 1 represents diaminopropionic
;     OTHER INFORMATION: acid (DAP)."
```

US-09-093-227-11

```

Query Match          100.0%; Score 110; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 PARVGLGITTVLMTTQSSGSRA 23
        |||||||||||||||||||
Db      2 PARVGLGITTVLMTTQSSGSRA 24
```

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	ID	
1	110	100.0	337	2	A49970	glycine receptor a
2	110	100.0	449	2	S12382	glycine receptor a
3	110	100.0	451	2	C49970	glycine receptor a
4	110	100.0	457	2	S20662	glycine receptor a
5	104	94.5	451	2	B49970	glycine receptor a
6	104	94.5	452	2	S14816	glycine receptor a
7	104	94.5	452	2	S12381	glycine receptor a
8	104	94.5	452	2	S18836	glycine receptor a
9	104	94.5	464	2	A23682	glycine receptor a
10	87	79.1	478	2	T24805	hypothetical prote
11	77	70.0	461	2	S50864	avermectin-sensiti
12	77	70.0	495	2	T20754	hypothetical prote
13	77	70.0	496	2	JN0603	gamma-aminobutyric
14	77	70.0	499	2	S17785	gamma-aminobutyric
15	77	70.0	533	2	S33744	cyclodiene insecti
16	77	70.0	1106	2	T25065	hypothetical prote
17	76	69.1	457	2	S38296	gamma-aminobutyric
18	76	69.1	465	2	A38079	gamma-aminobutyric
19	76	69.1	545	2	T27614	hypothetical prote
20	75	68.2	437	2	S34469	gamma-aminobutyric
21	74	67.3	449	2	A36303	gamma-aminobutyric
22	74	67.3	449	2	I52630	GABAA receptor del
23	74	67.3	449	2	A34625	gamma-aminobutyric
24	73	66.4	464	2	JH0824	gamma-aminobutyric
25	73	66.4	465	2	S12056	gamma-aminobutyric
26	73	66.4	466	2	JQ0077	gamma-aminobutyric
27	73	66.4	466	2	JH0316	gamma-aminobutyric
28	73	66.4	467	2	S03905	gamma-aminobutyric
29	73	66.4	474	2	JH0317	gamma-aminobutyric

30	73	66.4	474	2	S13086	gamma-aminobutyric
31	73	66.4	475	2	B39272	gamma-aminobutyric
32	71	64.5	210	2	JH0794	gamma-aminobutyric
33	71	64.5	464	2	S65756	gamma-aminobutyric
34	71	64.5	467	2	S16915	gamma-aminobutyric
35	71	64.5	467	2	S19317	gamma-aminobutyric
36	70	63.6	423	2	T19145	hypothetical prote
37	70	63.6	473	2	A38627	gamma-aminobutyric
38	70	63.6	601	2	T32486	hypothetical prote
39	68	61.8	474	2	B60039	gamma-aminobutyric
40	68	61.8	474	2	A40336	gamma-aminobutyric
41	68	61.8	474	2	S53530	gamma-aminobutyric
42	68	61.8	474	2	B27142	gamma-aminobutyric
43	67	60.9	443	2	S11396	gamma-aminobutyric
44	67	60.9	453	2	S11087	gamma-aminobutyric
45	67	60.9	552	2	S17551	gamma-aminobutyric

# RESULT 1

A49970

glycine receptor alpha-4 chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 20-Aug-1999

C;Accession: A49970

R;Matzenbach, B.; Maulet, Y.; Sefton, L.; Courtier, B.; Avner, P.; Guenet, J.L.; Betz, H. J. Biol. Chem. 269, 2607-2612, 1994

A;Title: Structural analysis of mouse glycine receptor alpha subunit genes.

Identification and chromosomal localization of a novel variant alpha4.

A;Reference number: A49970; MUID:94132024

A;Accession: A49970

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-337 <MAT>

A;Cross-references: GB:X75850; NID:g435513; PIDN:CAA53468.1; PID:g817957

C;Genetics:

A;Gene: Gla4

C;Superfamily: acetylcholine receptor

C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match 100.0%; Score 110; DB 2; Length 337;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PARVGLGITTTLMTTQSSGSRA 23

|||||

Db 261 PARVGLGITTTLMTTQSSGSRA 283

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	110	100.0	449	6	Q9GKF0	Q9gkf0 bos taurus
2	110	100.0	456	13	Q9DES9	Q9des9 brachydanio
3	110	100.0	457	6	Q9GKE9	Q9gke9 bos taurus
4	104	94.5	147	11	Q9JL29	Q9jl29 mus musculu
5	104	94.5	219	4	Q9UPF3	Q9upf3 homo sapien
6	104	94.5	480	11	Q99JC9	Q99jc9 rattus norv
7	87	79.1	416	5	Q17367	Q17367 caenorhabdi
8	87	79.1	421	5	O46123	O46123 haemonchus
9	87	79.1	478	5	O17548	O17548 caenorhabdi
10	87	79.1	654	5	O01436	O01436 caenorhabdi
11	87	79.1	657	5	O17547	O17547 caenorhabdi
12	87	79.1	657	5	Q9TW41	Q9tw41 caenorhabdi

13	86	78.2	351	5	Q25634	Q25634	onchocerca
14	84	76.4	379	5	O96964	O96964	ascaris suu
15	84	76.4	430	5	Q17369	Q17369	caenorhabdi
16	84	76.4	435	5	Q9TZR3	Q9tzt3	haemonchus
17	84	76.4	435	5	Q9TYG6	Q9tyg6	haemonchus
18	84	76.4	435	5	Q9GQW8	Q9gqw8	haemonchus
19	84	76.4	438	5	O46124	O46124	haemonchus
20	84	76.4	484	5	Q9U990	Q9u990	caenorhabdi
21	81	73.6	336	5	Q9GQ52	Q9gq52	drosophila
22	81	73.6	452	5	O76773	O76773	lucilia cup
23	81	73.6	453	5	O77295	O77295	drosophila
24	81	73.6	454	5	Q9VDU5	Q9vdu5	drosophila
25	81	73.6	456	5	Q94900	Q94900	drosophila
26	81	73.6	456	5	Q9GQ53	Q9gq53	drosophila
27	77	70.0	57	5	Q9TX49	Q9tx49	drosophila
28	77	70.0	77	5	O18470	O18470	heliothis v
29	77	70.0	141	5	Q26435	Q26435	tribolium c
30	77	70.0	254	5	Q26410	Q26410	blattella g
31	77	70.0	256	5	Q26409	Q26409	blattella g
32	77	70.0	274	5	Q26411	Q26411	blattella g
33	77	70.0	276	5	Q26412	Q26412	blattella g
34	77	70.0	365	5	O77249	O77249	apis mellif
35	77	70.0	444	5	O76472	O76472	musca domes
36	77	70.0	461	5	O17793	O17793	caenorhabdi
37	77	70.0	475	5	Q9Y0I4	Q9y0i4	caenorhabdi
38	77	70.0	481	5	O18471	O18471	heliothis v
39	77	70.0	486	5	Q9GYU4	Q9gyu4	sepia offic
40	77	70.0	487	5	Q9Y0I5	Q9y0i5	caenorhabdi
41	77	70.0	494	5	Q9XZW0	Q9xzw0	heliothis v
42	77	70.0	496	5	O18468	O18468	heliothis v
43	77	70.0	506	5	Q9Y0I3	Q9y0i3	caenorhabdi
44	77	70.0	533	5	Q16896	Q16896	aedes aegyp
45	77	70.0	541	5	Q9U9B8	Q9u9b8	ceratitis c

30. A method of altering the flux of water across an epithelial cell presenting first and second spaced apart surfaces, said method comprising the steps of:

- a. providing a peptide capable of forming a channel assembly for transport of anions through said epithelial cell, each of said peptides having at least about 35% sequence homology with a peptide selected from the group consisting of SEQ ID Nos. 4-47; and
- b. contacting said peptide with said first surface of said epithelial cell, and causing said peptide to alter the flux of water across said cell surface.

31. The method of claim 30, said peptide having at least about 50% sequence homology with a peptide selected from the group consisting of SEQ ID Nos. 4-47.

32. The method of claim 31, said peptide having at least about 65% sequence homology with a peptide selected from the group consisting of SEQ ID Nos. 4-47.

33. The method of claim 30, said peptide being substantially monomeric in solution.

34. The method of claim 30, said peptide being soluble to a level of at least about 5 mM.

35. The method of claim 34, said peptide being soluble to a level of at least about 10 mM.

36. The method of claim 30, said peptide having at least about 50% helical content.

R128 <sup>40</sup>/<sub>42</sub>

A method of altering the flux of water across an epithelial cell presenting first and second spaced apart surfaces, said method comprising the steps of:

- a. providing a peptide capable of forming a channel assembly for transport of anions through said epithelial cell, said peptide having the sequence of SEQ ID NO. 18; and
- b. contacting said peptide with said first surface of said epithelial cell, and causing said peptide to alter the flux of water across said cell surface.

09710 419

11-9-2000

18. (Amended) A method of decreasing resistivity of a cell layer comprising the step of contacting said cell layer with a peptide, said peptide being a derivative of SEQ ID No. 1.

19. The method of claim 18, said cell layer comprising MDCK cells.

20. (Amended) The method of claim 46, said palindromic portion comprising at least seven amino acid residues.

21. The method of claim 20, said palindromic portion comprising at least about 9 amino acid residues.

22. The method of claim 21, said palindromic portion comprising at least about 11 amino acid residues.

23. The method of claim 18, said peptide being modified to contain a plurality of polar amino acid residues at the C-terminus, the N-terminus, or the C- and N-terminus of said peptide.

24. The method of claim 23, said polar amino acid residues comprising lysine.

25. The method of claim 18, said peptide being present at a concentration of at least about 500  $\mu$ M.

26. The method of claim 25, said peptide being present at a concentration of at least about 300  $\mu$ M.

27. The method of claim 18, said derivative having at least about 35% sequence homology with a peptide sequence selected from the group consisting of SEQ ID Nos. 4-47.

28. The method of claim 18, said peptide having at least about 50% helical content.

29. The method of claim 18, said peptide being substantially monomeric in solution.

30. A method of altering the flux of water across an epithelial cell presenting first and second spaced apart surfaces, said method comprising the steps of:

a. providing a peptide capable of forming a channel assembly for transport of anions through said epithelial cell, each of said peptides having at least about 35% sequence homology with a peptide selected from the group consisting of SEQ ID Nos. 4-47; and

b. contacting said peptide with said first surface of said epithelial cell, and causing said peptide to alter the flux of water across said cell surface.

31. The method of claim 30, said peptide having at least about 50% sequence homology with a peptide selected from the group consisting of SEQ ID Nos. 4-47.

32. The method of claim 31, said peptide having at least about 65% sequence homology with a peptide selected from the group consisting of SEQ ID Nos. 4-47.

33. The method of claim 30, said peptide being substantially monomeric in solution.

34. The method of claim 30, said peptide being soluble to a level of at least about 5 mM.

35. The method of claim 34, said peptide being soluble to a level of at least about 10 mM.

36. The method of claim 30, said peptide having at least about 50% helical content.

41. A method of altering the flux of water from an epithelial cell comprising the steps of:

providing multiple peptides capable of forming a channel assembly, each of said peptides having from about 16-31 amino acid residues therein and selected from the group consisting of derivatives of SEQ ID No. 1; and contacting said epithelial cell with said peptides.

42. The method of claim 41, said epithelial cells selected from the group consisting of airway, intestinal, pancreatic duct, and epididymus epithelial cells.

43. The method of claim 42, said epithelial cell being airway epithelial cells and said method further comprising the step of aerosolizing said peptides.

44. The method of claim 41, said contacting step including the step of causing said peptides to embed in said epithelial cell.

45. The method of claim 41, said contacting step including the step of causing said epithelial cell layer resistivity to decrease.

46. The method of claim 18, said derivative including at least one portion which is palindromic to a portion of SEQ ID No. 1.

nd  
scf

n.e.

3

n.e.

SEQ ID NO. 13 22 A.A.

## Murphy, Joseph

---

**Fr m:** Murphy, Joseph  
**Sent:** Wednesday, June 05, 2002 10:55 AM  
**T :** STIC-Biotech/ChemLib  
**Subject:** 09710419

STIC/Biotech:

Please search SEQ ID NO: 1 against protein databases.

Please include an interference search of SEQ ID NO: 1.

Please search for 31 contigs of SEQ ID NO: 1.

Please search for 16 contigs of SEQ ID NO: 1.

Please send the results on DISK.

Thanks a lot.

Joseph F. Murphy, Ph.D.  
Patent Examiner, Art Unit 1646  
joseph.murphy@uspto.gov  
CM1 9A01  
Mailbox: 10C01  
(703) 305-7245